Attachment Paper 25

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan et al.	
	FILING DATE November 10, 2000	GROUP 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
NONE							

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
NONE								

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

JBB	A	Koehl *et al.*, "A brighter future for protein structure prediction", *Nature Structure Biology*, 6(2):108-111, 1999
JBB	B	Sternberg *et al.*, "Progress in protein structure prediction: assessment of CASP3", *Current Opinion in Structural Biology*, 9:368-373, 1999

EXAMINER John S. Brusca | DATE CONSIDERED 11/27/02

EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

attachment to Paper 19

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan *et al.*	
	FILING DATE November 10, 2000	GROUP 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
JB	AA	9514791	06/01/95	PCT				

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

		None

EXAMINER	J.B. Brunsa	DATE CONSIDERED	11/27/02

EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Title: **USE OF COMPUTATIONALLY DERIVED PROTEIN STRUCTURES OF GENETIC POLYMORPHISMS IN PHARMACOGENOMICS FOR DRUG DESIGN AND CLINICAL APPLICATIONS**

attachment Paper 17

FORM PTO 1449 (Modified)

LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT

ATTY. DOCKET NO.	SERIAL NO.
24737-1906C	09/709,905
APPLICANT: Ramnarayan *et al.*	
FILING DATE: November 10, 2000	GROUP: 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
JSB	A	5 3 3 1 5 7 3	07/19/94	Balaji *et al.*			

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
JSB	B	9 5 0 6 2 9 3	03/02/95	PCT				
JSB	C	9 5 1 4 0 2 8	05/26/95	PCT				
JSB	D	9 8 0 6 0 4 8	02/12/98	PCT				
JSB	E	9 8 1 3 7 8 1	04/02/98	PCT				
JSB	F	9 8 5 4 6 6 5	12/03/98	PCT				

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

JSB	G /	Abdel-Meguid, S.S. *et al.* "An orally bioavailable HIV-1 protease inhibitor containing an imidazole-derived peptide bond replacement: crystallographic and pharmacokinetic analysis," *Biochemistry* 33(39):11671-11677 (1994)
	H	Blaney, R. "Molecular modelling in the pharmaceutical industry. *Chemistry and Industry. Chemistry and Industry Review* 23(4):791-4 (1990). not considered no copy provided
	I	Bohm,G. "New approaches in molecular structure prediction" *Biophysical Chemsitry* 59:1-32 (1996) not considered no copy provided
JSB	J /	Thompson, S.K. *et al.* "Rational design, synthesis, and crystallographic analysis of a hydroxyethylene-based HIV-1 protease inhibitor containing a heterocyclic P1'-P2' amide bond isoster," *Journal of Medicinal Chemistry* 37(19):3100-3107 (1994).

EXAMINER J.S. Brusca | DATE CONSIDERED 11/27/02

EXAMINER: Initial if citation considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Attachment Paper 21

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan *et al.*	
	FILING DATE November 10, 2000	GROUP 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
* JBB	AA	5 3 1 7 0 9 7	05/31/94	Miller *et al.*	~~536~~	~~24.31~~	10/07/91
* JBB	AB	5 4 9 5 4 2 3	02/27/96	DeLisi *et al.*	~~364~~	~~496~~	10/25/93
* JBB	AC	5 5 9 3 9 5 9	01/14/97	Miller *et al.*	~~514~~	8	10/14/93
* JBB	AD	5 6 2 4 8 1 7	04/29/97	Miller *et al.*	~~435~~	69.1	04/28/94
* JBB	AE	5 6 9 9 2 6 8	12/16/97	Schmidt	~~364~~	~~496~~	06/07/95
* JBB	AF	5 9 6 8 7 3 7	10/19/99	Ali-Osman *et al.*	~~435~~	6	11/12/96
* JBB	AG	5 9 7 8 7 4 0	11/02/99	Armistead *et al.*	~~702~~	~~19~~	08/09/95
* JBB	AH	6 1 2 8 5 8 2	10/03/00	Wilson *et al.*	~~702~~	~~27~~	04/30/96

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
None								

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* JBB	AI	Baker *et al.*, "Protein Structure Prediction and Structural Genomics", Science, 294:93-96 (2001)
* JBB	AJ	Hess *et al.*, "Impact of Pharmacogenomics on the Clinical Laboratory", *Mol. Diagn.*, 4(4):289-98 (1999)
* JBB	AK	Hess *et al.*, "Gene Therapy Monitoring: Clinical Monitoring for Efficacy and Potential Toxicity, *Mol. Diagn.*, 2(2):147-155 (1997)

EXAMINER	J. B. Brusca	DATE CONSIDERED	11/27/02

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Title: **USE OF COMPUTATIONALLY DERIVED PROTEIN STRUCTURES OF GENETIC POLYMORPHISMS IN PHARMACOGENOMICS FOR DRUG DESIGN AND CLINICAL APPLICATIONS**

Attachment # Paper 16

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan *et al.*	
	FILING DATE November 10, 2000	GROUP 1631

* References are not included.

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER							DATE	NAME	CLASS	SUB CLASS	FILING DATE
*	AA	5	7	1	2	1	4	5	01/27/98	Houghton *et al.*	~~435~~	~~219~~	09/06/96

FOREIGN PATENT DOCUMENTS

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*	AB	Ajay *et al.*, Computational Methods to Predict Binding Free Energy in Ligand-Receptor Complexes, Journal of Medicinal Chemistry. 38(26):4953-4967 (1995).
*	AC	Balaji *et al.*, Conformational studies on model peptides with 1-aminocyclopropane 1-carboxylic acid residues, Pept. Res. 7(2):60-71 (1994).
*	AD	Balaji *et al.*, Conformational studies on model peptides with 1-aminocyclobutane 1-carboxylic acid residues, Pept. Res. 8(3):178-86 (1995).
*	AE	Balasubramaniam *et al.*, [D-TRP^{32}]Neuropeptide Y: A Competitive Antagonist of NPY in Rat Hypothalamus, J. Med. Chem. 37(6):811-815 (1994).
*	AF	Böhm, Prediction of binding constants of protein ligands: A fast method for the prioritization of hits obtained from de novo design or 3D database search programs, Journal of Computer-Aided Molecular Design. 12:309-323 (1998).
*	AG	Checa *et al.*, Assessment of Solvation Effects on Calculated Binding Affinity Differences: Trypsin Inhibition by Flavonoids as a Model System for Congeneric Series, J. Med. Chem. 40:4136-4145 (1997).
*	AH	Daniels, Blood group polymorphisms: molecular approach and biological significance, Transfus. Clin. Biol. 4:383-390 (1997).

Duplicate

EXAMINER J. S. Bruce | DATE CONSIDERED 11/27/02

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	FILING DATE November 10, 2000	GROUP 1631

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

*	AI	Das *et al.*, Crystal Structures of 8-Cl and 9-Cl Complexed with Wild-type HIV-1 RT and 8-Cl TIBO Complexed with the Tyr181Cys HIV-1 RT Drug-resistant Mutant, J. Mol. Biol. 264:1085-1100 (1996).
*	AJ	Eldridge *et al.*, Empirical scoring functions: I. The development of a fast empirical scoring function to estimate the binding affinity of ligands in receptor complexes, Journal of Computer-Aided Molecular Design. 11:425-445 (1997).
*	AK	Fox, S. Pharmacogenomics Thrives in Europe. Genetic Engineering News. June 15, 1999.
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*	AM	Manavalan *et al.*, Location of Potential Binding Sites on Deoxy Hemoglobin for the Design of Antigelling Agents, J. Mol. Biol. 223:791-800 (1992).
*	AN	Munson *et al.*, Identification of an extracytoplasmic region of H+, K(+)- ATPase labeled by a K(+)-competitive photoaffinity inhibitor, J. Biol. Chem. 266(28):18976-88 (1991).
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*	AP	Press Release, Structural Bioinformatics Inc. and Cyberchemics, Inc. Collaborate to Speed the Generation of Hepatitis C Viral Protease Inhibitors, SBI News. Located at http://strubix.com/press/press5.html, pp. 1-2 (1997).
*	AQ	Press Release, Structural Bioinformatics Inc. Selects IBM RS/6000 SP to Spee Drug Design, SBI News. Located at http://strubix.com/press/press11.html, pp.1-2 (1997).
*	AR	Press Release, SBI Protein Models & Ligand Binding for Novel Viral Enzyme Validated, SBI News. Located at http://strubix.com/press/press32.html, pp. 1-2 (1999).
*	AS	Press Release, Structural Bioinformatics Inc. Generates Antiviral Lead Compound from Gene Sequence to Achieve Milestone in Biochem Pharma Collaboration, SBI News. Located at http://strubix.com/press/press20.html, pp. 1-2 (1998).
*	AT	Press Release, SBI's Protein Structure Directed Combinatorial Chemistry Cuts Time and Cost 100X for Synthesis of New Anti-Inflammatory Drug Lead Molecules (TNF Receptor Antagonists), SBI News. Located at http://strubix.com/press/press19.html, pp. 1-2 (1998).

EXAMINER	DATE CONSIDERED
J.S. Brusca	11/27/02

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	FILING DATE November 10, 2000	GROUP 1631

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

*	AU	Press Release, Structural Bioinformatics Inc. Generates Non-Peptide Lead Molecules Active Against the EPO Receptor from Gene Sequence Data, SBI News. Located at http://strubix.com/press/press22.html, pp. 1-2 (1998).
*	AV	Press Release, Structural Bioinformatics Inc. Develops Small-Molecule Antagonists of BCL-2 Gene Product, an Important Apoptosis-Related Protein Target in the Pathology of Human Cancers, SBI News. Located at http://strubix.com/press/press26.html, pp. 1-2 (1999)
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*	AX	Radmer *et al.*, The application of three approximate free energy calculations methods to structure based ligand design: Trypsin and its complex with inhibitors, Journal of Computer-Aided Molecular Design. 12:215-227 (1998).
*	AY	Ramnarayan *et al.*, Antibody humanization predicted by computer graphic analysis, Am. Biotechnol. Lab. 13(9):26,28 (1995).
*	AZ	Ramnarayan *et al.*, Conformational studies on model dipeptides of Gly, L-Ala and their C^{α}-substituted analogs, Int. J. Pept. Protein Res. 45(4):366-76 (1995).
*	BA	Ramnarayan *et al.*, Characterization of a Linear Pentapeptide Containing Two Consecutive β-Turns, Pept. Res. 7(5):270-8 (1994).
*	BB	Regalado, Inventing the pharmacogenomics business, Am. J. Health-Syst. Pharm. 56:40-50 (1999).
*	BC	Rao *et al.*, Conformational Studies on β-Amino Acid-Containing Peptides. I., Pept. Res. 5(6):343-50 (1992).
*	BD	Shafer *et al.*, Multiple Concurrent Reverse Transcriptase and Protease Mutations and Multidrug Resistance of HIV-1 Isolates from Heavily Treated Patients, Annals of Internal Medicine. 128(11):906-11 (1998).
*	BE	Skaletsky *et al.*, Accessing three-dimensional chemical information in antibody molecules, Am. Biotechnol. Lab. 11(5):10-3 (1993).
*	BF	~~Shenderovich, *et al.*, "Structural Pharmacogenic Approach to the Evaluation of Drug Resistant Mutations and HIV-1 Protease", *Journal of Clinical Ligand Assay*, 24(2):140-144 (2001)~~ not considered no copy provided

EXAMINER J.S. Brusca | DATE CONSIDERED 11/27/02

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	FILING DATE November 10, 2000	GROUP 1631

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

* JB	BG	Smith *et al.*, Molecular modeling of HIV-1 reverse transcriptase drug-resistant mutant strains: implications for the mechanism of polymerase action, Protein Engineering. 10(12):1379-83 (1997). Duplicate
*	BH	Spear, Viewpoint - Pharmacogenomics: Today, Tomorrow, and Beyond, Drug Benefit Trends. 11(2):53-54 (1999).
*	BI	Takamatsu *et al.*, A New Method for Predicting Binding Free Energy Between Receptor and Ligand, Proteins: Structure, Function, and Genetics. 33:62-73 (1998).
*	BJ	Tantillo *et al.* Locations of Anti-AIDS Drug Binding Sites and Resistance Mutations in the Three-dimensional Structure of HIV-1 Reverse Transcriptase, J. Mol. Biol. 243:369-387 (1994).
*	BK	Vajda *et al.* Empirical potentials and functions for protein folding and binding, Theory and Simulation. 7:222-228 (1997).
*	~~BL~~	~~Wang and Kollman, "Computational study of protein specificity: The molecular basis of HIV-1 protease drug resistance", *PNAS*, 98(26):14937-14942 (2001).~~ not considered no copy provided
*	~~BM~~	~~Weng *et al.*, Prediction of protein complexes using empirical free energy functions, Protein Science. 5:614-626 (1996).~~ not considered no copy provided
* JB	BN	Zhu *et al.*, Identification of two new hydrophobic residues on basic fibroblast growth factor important for fibroblast growth factor receptor binding, Protein Engineering 11(10):937-40 (1998). Duplicate
*	BO	Zhu *et al.*, Analysis of high-affinity binding determinants in the receptor binding epitope of basic fibroblast growth factor, Protein Eng. 10(4):417-21 (1997).
*	BP	Zhu *et al.*, Glu-96 of basic fibroblast growth factor is essential for high affinity receptor binding. Identification by structure-based site-directed mutagenesis, J. Biol. Chem. 270(37):21869-74 (1995).

EXAMINER	J.B. Brusca	DATE CONSIDERED	11/27/02

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attachment Paper 12

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24727-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan *et al.*	
	FILING DATE November 20, 2000	GROUP 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE

FOREIGN PATENT DOCUMENTS

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
JB		0 1 3 5 3 1 6	05/17/01	PCT				

OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

EXAMINER J.K. Bruce | DATE CONSIDERED 11/26/02

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attachment Paper 3

FORM PTO-1449 (Modified)	ATTY. DOCKET NO. 24737-1906C	SERIAL NO. 09/709,905
LIST OF PATENTS AND PUBLICATIONS FOR APPLICANT'S INFORMATION DISCLOSURE STATEMENT	APPLICANT Ramnarayan *et al.*	
	FILING DATE November 10, 2000	GROUP ~~2857~~ 1631

U.S. PATENT DOCUMENTS

EXAMINER INITIAL		DOCUMENT NUMBER	DATE	NAME	CLASS	SUB CLASS	FILING DATE
* JBB		4 2 0 8 4 7 9	06/17/80	Zuk *et al.*	~~435~~	7	07/14/77
* JBB		4 2 2 0 4 5 0	09/02/80	Maggio	~~23~~	~~230~~	04/05/78
* JBB		4 2 3 3 4 0 1	11/11/80	Yoshida *et al.*	~~435~~	~~7~~	07/14/77
* JBB		4 2 3 3 4 0 2	11/11/80	Maggio *et al.*	~~435~~	~~7~~	04/05/78
* JBB		4 2 7 7 4 3 7	07/01/81	Maggio	~~422~~	~~61~~	12/10/79
* JBB		4 3 8 5 1 2 6	05/24/83	Chen *et al.*	~~436~~	~~518~~	03/19/79
* JBB		4 3 9 7 9 5 6	08/09/83	Maggio	~~436~~	~~34~~	12/10/81
* JBB		4 7 8 6 4 7 1	11/22/88	Jones *et al.*	~~422~~	~~61~~	10/21/83
* JBB		4 7 8 9 6 3 1	12/06/88	Maggio	~~435~~	~~7~~	02/17/84
* JBB		4 8 2 8 9 8 1	05/09/89	Maggio	~~435~~	~~7~~	08/24/83
* JBB		4 8 5 9 6 1 0	08/22/89	Maggio	~~436~~	~~518~~	09/12/86
* JBB		5 0 7 9 1 4 2	01/07/92	Coleman *et al.*	435	7.92	01/23/87
* JBB		5 2 1 5 8 9 9	06/01/93	Dattagupta	435	6	08/23/90
* JBB		5 3 3 1 5 7 3	07/19/94	Balaji *et al.*	~~364~~	~~500~~	12/14/90
* JBB		5 5 7 1 8 2 1	11/05/96	Chan *et al.*	~~514~~	~~312~~	05/20/94
* JBB		5 5 7 9 2 5 0	11/26/96	Balaji *et al.*	~~364~~	~~496~~	04/24/95
* JBB		5 6 1 2 8 9 5	03/18/97	Balaji *et al.*	~~364~~	~~496~~	04/21/95
* JBB		5 7 1 2 1 4 5	01/27/98	Houghton *et al.*	~~435~~	~~219~~	09/06/96
* JBB		5 8 0 8 9 6 9	09/15/98	Arnaud *et al.*	~~367~~	~~103~~	12/04/95
* JBB		5 8 3 7 4 6 4	11/17/98	Capon *et al.*	~~435~~	~~6~~	01/29/97
* JBB		5 8 4 6 7 6 3	12/08/98	Lee *et al.*	~~435~~	~~69.1~~	05/13/94
* JBB		5 9 1 0 4 7 8	06/08/99	Hlavka *et al.*	~~514~~	~~9~~	09/20/96

FOREIGN PATENT DOCUMENTS

EXAMINER J.B. Brunsman | DATE CONSIDERED 11/26/02

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	FILING DATE November 10, 2000	GROUP ~~2857~~ 1631

		DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUB CLASS	Translation Yes	Translation No
*		00573097	09/28/00	PCT				
*		97273197	07/31/97	PCT				
*		97274804	07/31/97	PCT				
*		99065975	02/11/99	PCT				

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*		~~*3D QSAR in Drug Design* Kubinyi, H (ed.) Kluwer Academic Publishers (1993).~~ Not considered no copy provided
*		Abagyan *et al.* Biased Probability Monte Carlo Conformational Searches and Electrostatic Calculations for Peptides and Proteins, *J. Mol. Biol.* 235: 983-1002 (1994).
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*		Altschul *et al.* Basic Local Alignment Search Tool, *J. Mol. Biol.* 215: 403-10 (1990).
*		Balaji *et al.*, Conformational studies on model peptides with 1-aminocyclopropane 1-carboxylic acid residues, Pept. Res. 7(2):60-71 (1994).
*		Balaji *et al.*, Conformational studies on model peptides with 1-aminocyclobutane 1-carboxylic acid residues, Pept. Res. 8(3):178-86 (1995).
*		Balasubramaniam *et al.*, [D-TRP^{32}]Neuropeptide Y: A Competitive Antagonist of NPY in Rat Hypothalamus, J. Med. Chem. 37(6):811-815 (1994).
*		Balasubramanian, R., New type of representation for mapping chain-folding in protein molecules, *Nature* 266: 856-57 (1977).
*		Bernstein *et al.*, The protein data bank: a computer-based archival file for macromolecule structures, J. Mol. Biol., 112:535-542 (1977)

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OTHER ART (Including Author, Title, Date, Pertinent Pages, Etc.)

*		~~*Biocomputing: Informatics and Genome Projects* Smith, D.W., ed. Academic Press, Inc., San Diego (1994).~~ NOT considered no copy provided
*	JSB	Böhm, Prediction of binding constants of protein ligands: A fast method for the prioritization of hits obtained from de novo design or 3D database search programs, Journal of Computer-Aided Molecular Design. 12:309-323 (1998).
*	JSB	Bouras *et al.* Design, Synthesis, and Evaluation of Conformationally Constrained Tongs, New Inhibitors of HIV-1 Protease Dimerization, *42:* 957-62 (1999).
*	JSB	Carrillo, H. and D. Lipman., The Multiple Sequence Alignment Problem in Biology, *SIAM J. Appl. Math.* 48(5): 1073-82 (1988).
*	JSB	Carson and Bugg, Algorithm for ribbon models of proteins, J. Mol. Graphics, 4:121-122 (1986)
*	JSB	Carson, Ribbons 2.0, J. Appl. Cryst., 24:958-961 (1991)
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